

**EXHIBIT A**



60240 SeqList 10.14.05.ST25  
SEQUENCE LISTING

<110> The Trustees of Columbia University in the City of New York  
Trakht, Ilya  
Canfield, Robert  
Kalantarov, Gary  
Rudchenko, Sergei

<120> Novel Tumor-Associated Marker

<130> 0575/60240/JPW/AJM/AJD

<140> 09/664,958

<141> 2000-09-28

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<170> PatentIn version 3.3

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Ser Ala His Val Ser Gly Arg Val Val Met Lys Ser Tyr Leu Ser Gly  
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Val Lys Arg Leu Asn Gly Ile Cys Ala Gln Val Leu Pro Tyr Leu Ser  
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Lys Leu Ala Ser Glu Lys Ser Glu Met Gln Arg His Tyr Val Met Tyr  
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Tyr Glu Met Ser Tyr Gly Leu Asn Ile Glu Met His Lys Gln Ala Glu  
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Ile Val Lys Arg Leu Asn Gly Ile Cys Ala Gln Val Leu Pro Tyr Leu  
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Ser Gln Glu His Gln Gln Gln Val Leu Gly Ala Ile Glu Arg Ala Lys  
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## 60240 SeqList 10.14.05.ST25

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Ala His Gln Leu Ser Gln Leu Gln Ala Leu Ala Leu Pro Leu Thr Pro  
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Leu Pro Val Gly Leu Gln Pro Pro Ser Leu Pro Ala Val Ser Ala Gly  
 145 150 155 160

Thr Gly Leu Leu Ser Leu Ser Ala Leu Gly Ser Gln Ala His Leu Ser  
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Lys Lys Ala Arg Glu Ala Trp Lys Ile Trp Ala Asp Ile Pro Ala Pro  
65 70 75 80

Lys Arg Gly Glu Ile Val Arg Gln Ile Gly Asp Ala Leu Arg Glu Lys  
85 90 95

Ile Gln Val Leu Gly Ser Leu Val Ser Leu Glu Met Gly Lys Ile Leu  
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100

105

110

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ctccctcaaa aaggggaggg acagatgggg agcttttctt acctattcaa ggaatacgtg   1380
cctttttctt aaatgctttc atttattgaa aaaaaaaaaa aaaaaaaaaa   1428

```

```

<210> 22
<211> 372
<212> PRT
<213> Human

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```
<400> 22
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```
Met Ala Tyr His Ser Phe Leu Val Glu Pro Ile Ser Cys His Ala Trp
1          5          10          15
```

```
Asn Lys Asp Arg Thr Gln Ile Ala Ile Cys Pro Asn Asn His Glu Val
          20          25          30
```

```
His Ile Tyr Glu Lys Ser Gly Ala Lys Trp Thr Lys Val His Glu Leu
          35          40          45
```

```
Lys Glu His Asn Gly Gln Val Thr Gly Ile Asp Trp Ala Pro Glu Ser
          50          55          60
```

```
Asn Arg Ile Val Thr Cys Gly Thr Asp Arg Asn Ala Tyr Val Trp Thr
65          70          75          80
```

```
Leu Lys Gly Arg Thr Trp Lys Pro Thr Leu Val Ile Leu Arg Ile Asn
          85          90          95
```

Arg Ala Ala Arg Cys Val Arg Trp Ala Pro Asn Glu Asn Lys Phe Ala  
 100 105 110  
 Val Gly Ser Gly Ser Arg Val Ile Ser Ile Cys Tyr Phe Glu Gln Glu  
 115 120 125  
 Asn Asp Trp Trp Val Cys Lys His Ile Lys Lys Pro Ile Arg Ser Thr  
 130 135 140  
 Val Leu Ser Leu Asp Trp His Pro Asn Asn Val Leu Leu Ala Ala Gly  
 145 150 155 160  
 Ser Cys Asp Phe Lys Cys Arg Ile Phe Ser Ala Tyr Ile Lys Glu Val  
 165 170 175  
 Glu Glu Arg Pro Ala Pro Thr Pro Trp Gly Ser Lys Met Pro Phe Gly  
 180 185 190  
 Glu Leu Met Phe Glu Ser Ser Ser Ser Cys Gly Trp Val His Gly Val  
 195 200 205  
 Cys Phe Ser Ala Ser Gly Ser Arg Val Ala Trp Val Ser His Asp Ser  
 210 215 220  
 Thr Val Cys Leu Ala Asp Ala Asp Lys Lys Met Ala Val Ala Thr Leu  
 225 230 235 240  
 Ala Ser Glu Thr Leu Pro Leu Leu Ala Leu Thr Phe Ile Thr Asp Asn  
 245 250 255  
 Ser Leu Val Ala Ala Gly His Asp Cys Phe Pro Val Leu Phe Thr Tyr  
 260 265 270  
 Asp Ala Ala Ala Gly Met Leu Ser Phe Gly Gly Arg Leu Asp Val Pro  
 275 280 285  
 Lys Gln Ser Ser Gln Arg Gly Leu Thr Ala Arg Glu Arg Phe Gln Asn  
 290 295 300  
 Leu Asp Lys Lys Ala Ser Ser Glu Gly Gly Thr Ala Ala Gly Ala Gly  
 305 310 315 320  
 Leu Asp Ser Leu His Lys Asn Ser Val Ser Gln Ile Ser Val Leu Ser  
 325 330 335  
 Gly Gly Lys Ala Lys Cys Ser Gln Phe Cys Thr Thr Gly Met Asp Gly  
 340 345 350

## 60240 SeqList 10.14.05.ST25

Gly Met Ser Ile Trp Asp Val Lys Ser Leu Glu Ser Ala Leu Lys Asp  
 355 360 365

Leu Lys Ile Lys  
 370

<210> 23  
 <211> 1435  
 <212> DNA  
 <213> Human

<400> 23  
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 caggaagtac ttcgagggct tcggcgacat cgaggaggcc gtggtcatca ccgaccgcca 180  
 gacgggcaag tcccgcggct acggcttcgt gaccatggcc gaccgggcgg cagctgagag 240  
 ggcttgcaaa gaccctaacc ccatcatcga cggccgcaag gccaacgtga acctggcata 300  
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 cccaccttg atccagcggg cttacgggct gaccccgcac tacatctacc caccagccat 420  
 cgtgcagcca agcgtggtga tcccagccgc ccctgtcccg tcgctgtcct cgccctacat 480  
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 gccgcagctg cagcctgaca ggatgcagtg agggggcgtt ctgccccgag gactgtggca 720  
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 cgccctggga cagcggagag acggcttctc tttaatctag gtccattgt gtcttgaggg 900  
 aggactttta agaattgactg agaactatct aaagacgcaa tcccagggtc cttgcacacc 960  
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 atagcactga agttgcaact tttttcttgt aattgttttg ctactaagat aatttcagaa 1380  
 gttcagtcta ttttttcagc ggatactgcc gccaccaaga atccaaacct aggaa 1435

## 60240 SeqList 10.14.05.ST25

<210> 24  
 <211> 230  
 <212> PRT  
 <213> Human

<400> 24

Ser Ala Gly Phe Ser Arg Pro Leu Ala Ala Pro Gly Val Met Tyr Gly  
 1 5 10 15

Ser Gln Lys Gly Thr Thr Phe Thr Lys Ile Phe Val Gly Gly Leu Pro  
 20 25 30

Tyr His Thr Thr Asp Ala Ser Leu Arg Lys Tyr Phe Glu Gly Phe Gly  
 35 40 45

Asp Ile Glu Glu Ala Val Val Ile Thr Asp Arg Gln Thr Gly Lys Ser  
 50 55 60

Arg Gly Tyr Gly Phe Val Thr Met Ala Asp Arg Ala Ala Ala Glu Arg  
 65 70 75 80

Ala Cys Lys Asp Pro Asn Pro Ile Ile Asp Gly Arg Lys Ala Asn Val  
 85 90 95

Asn Leu Ala Tyr Leu Gly Ala Lys Pro Trp Cys Leu Gln Thr Gly Phe  
 100 105 110

Ala Ile Gly Val Gln Gln Leu His Pro Thr Leu Ile Gln Arg Thr Tyr  
 115 120 125

Gly Leu Thr Pro His Tyr Ile Tyr Pro Pro Ala Ile Val Gln Pro Ser  
 130 135 140

Val Val Ile Pro Ala Ala Ala Pro Val Pro Ser Leu Ser Ser Pro Tyr  
 145 150 155 160

Ile Glu Tyr Thr Pro Ala Ser Pro Val Tyr Ala Gln Tyr Pro Pro Ala  
 165 170 175

Thr Tyr Asp Gln Tyr Pro Tyr Ala Ala Ser Pro Ala Thr Ala Asp Ser  
 180 185 190

Phe Val Gly Tyr Ser Tyr Pro Ala Ala Val His Gln Ala Leu Ser Ala  
 195 200 205

Ala Ala Pro Ala Gly Thr Thr Phe Val Gln Tyr Gln Ala Pro Gln Leu  
 210 215 220

## 60240 SeqList 10.14.05.ST25

Gln Pro Asp Arg Met Gln  
225 230

<210> 25  
<211> 1439  
<212> DNA  
<213> Human

<400> 25  
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gctcaggaag tacttcgagg gcttcggcga catcgaggag gccgtggtca tcaccgaccg 180  
ccagacgggc aagtcccgcg gctacggctt cgtgaccatg gccgaccggg cggcagctga 240  
gagggccttg aaagaccctt aaccccatca tcgacggccg caaggccaac gtgaacctgg 300  
catatctggg cgccaagcct tgggtgtctcc agacgggctt tgccattggc gtgcagcagc 360  
tgcacccac cttgatccag cggacttacg ggctgacccc gcactacatc taccaccag 420  
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gagctcccag gcgcacaggg gccgccggtg acaggggccc cggccaaag gcccctttcc 1320  
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<210> 26  
<211> 230  
<212> PRT



&lt;213&gt; Human

&lt;400&gt; 26

Arg Arg Met Gln Tyr Asn Arg Arg Phe Val Asn Val Val Pro Thr Phe  
 1 5 10 15

Gly Lys Lys Lys Gly Thr Thr Phe Thr Lys Ile Phe Val Gly Gly Leu  
 20 25 30

Pro Tyr His Thr Thr Asp Ala Ser Leu Arg Lys Tyr Phe Glu Gly Phe  
 35 40 45

Gly Asp Ile Glu Glu Ala Val Val Ile Thr Asp Arg Gln Thr Gly Lys  
 50 55 60

Ser Arg Gly Tyr Gly Phe Val Thr Met Ala Asp Arg Ala Ala Ala Glu  
 65 70 75 80

Arg Ala Cys Lys Asp Pro Asn Pro Ile Ile Asp Gly Arg Lys Ala Asn  
 85 90 95

Val Asn Leu Ala Tyr Leu Gly Ala Lys Pro Trp Cys Leu Gln Thr Gly  
 100 105 110

Phe Ala Ile Gly Val Gln Gln Leu His Pro Thr Leu Ile Gln Arg Thr  
 115 120 125

Tyr Gly Leu Thr Pro His Tyr Ile Tyr Pro Pro Ala Ile Val Gln Pro  
 130 135 140

Ser Val Val Ile Pro Ala Ala Pro Val Pro Ser Leu Ser Ser Pro Tyr  
 145 150 155 160

Ile Glu Tyr Thr Pro Ala Ser Pro Val Tyr Ala Gln Tyr Pro Pro Ala  
 165 170 175

Thr Tyr Asp Gln Tyr Pro Tyr Ala Ala Ser Pro Ala Thr Ala Asp Ser  
 180 185 190

Phe Val Gly Tyr Ser Tyr Pro Ala Ala Val His Gln Ala Leu Ser Ala  
 195 200 205

Ala Ala Pro Ala Gly Thr Thr Phe Val Gln Tyr Gln Ala Pro Gln Leu  
 210 215 220

Gln Pro Asp Arg Met Gln  
 225 230

## 60240 SeqList 10.14.05.ST25

<210> 27  
 <211> 2029  
 <212> DNA  
 <213> 27

<400> 27  
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 ccgactccga gcagtctctg tccttcgacc cgagccccgc gccctttccg ggacccctgc 180  
 cccgcgggca gcgctgccaa cctgccggcc atggagaccc cgtcccagcg gcgcgccacc 240  
 cgcagcgggg cgaggccag ctccactccg ctgtcgccca cccgcatcac ccggctgcag 300  
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 agccgcgagg tgtccggcat caaggccgcc tacgaggccg agctcgggga tgcccgaag 480  
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 cagcatgagg accagggtgga gcagtataag aaggagctgg agaagactta ttctgccaag 1020  
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 gagctgcagc agtcgcgcat ccgcatcgac agcctctctg cccagctcag ccagctccag 1140  
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 cccagcccta cctcgcagcg cagccgtggc cgtgcttcct ctactcatc ccagacacag 1440  
 ggtgggggca gcgtcaccaa aaagcgcaa ctggagtcca ctgagagccg cagcagcttc 1500  
 tcacagcacg cacgcactag cgggcgcgtg gccgtggagg aggtggatga ggagggcaag 1560  
 tttgtccggc tgcgcaacaa gtccaatgag gaccagtcca tgggcaattg gcagatcaag 1620  
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## 60240 SeqList 10.14.05.ST25

gctgggcagg tggtgacgat ctgggctgca ggagctgggg ccacccacag cccccctacc 1740  
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atcaactcca ctggggaaga agtggccatg cgcaagctgg tgcgctcagt gactgtggtt 1860  
gaggacgacg aggatgagga tggagatgac ctgctccatc accaccatgt gagtggtagc 1920  
cgccgctgag gccgagcctg cactggggcc acccagccag gcctgggggc agcctctccc 1980  
cagcctcccc gtgccaaaaa tcttttcatt aaagaatggt tggaacttt 2029

<210> 28  
<211> 572  
<212> PRT  
<213> Human

<400> 28

Met Glu Thr Pro Ser Gln Arg Arg Ala Thr Arg Ser Gly Ala Gln Ala  
1 5 10 15

Ser Ser Thr Pro Leu Ser Pro Thr Arg Ile Thr Arg Leu Gln Glu Lys  
20 25 30

Glu Asp Leu Gln Glu Leu Asn Asp Arg Leu Ala Val Tyr Ile Asp Arg  
35 40 45

Val Arg Ser Leu Glu Thr Glu Asn Ala Gly Leu Arg Leu Arg Ile Thr  
50 55 60

Glu Ser Glu Glu Val Val Ser Arg Glu Val Ser Gly Ile Lys Ala Ala  
65 70 75 80

Tyr Glu Ala Glu Leu Gly Asp Ala Arg Lys Thr Leu Asp Ser Val Ala  
85 90 95

Lys Glu Arg Ala Arg Leu Gln Leu Glu Leu Ser Lys Val Arg Glu Glu  
100 105 110

Phe Lys Glu Leu Lys Ala Arg Asn Thr Lys Lys Glu Gly Asp Leu Ile  
115 120 125

Ala Ala Gln Ala Arg Leu Lys Asp Leu Glu Ala Leu Leu Asn Ser Lys  
130 135 140

Glu Ala Ala Leu Ser Thr Ala Leu Ser Glu Lys Arg Thr Leu Glu Gly  
145 150 155 160

Glu Leu His Asp Leu Arg Gly Gln Val Ala Lys Leu Glu Ala Ala Leu  
165 170 175

## 60240 SeqList 10.14.05.ST25

Gly Glu Ala Lys Lys Gln Leu Gln Asp Glu Met Leu Arg Arg Val Asp  
 180 185 190  
 Ala Glu Asn Arg Leu Gln Thr Met Lys Glu Glu Leu Asp Phe Gln Lys  
 195 200 205  
 Asn Ile Tyr Ser Glu Glu Leu Arg Glu Thr Lys Arg Arg His Glu Thr  
 210 215 220  
 Arg Leu Val Glu Ile Asp Asn Gly Lys Gln Arg Glu Phe Glu Ser Arg  
 225 230 235 240  
 Leu Ala Asp Ala Leu Gln Glu Leu Arg Ala Gln His Glu Asp Gln Val  
 245 250 255  
 Glu Gln Tyr Lys Lys Glu Leu Glu Lys Thr Tyr Ser Ala Lys Leu Asp  
 260 265 270  
 Asn Ala Arg Gln Ser Ala Glu Arg Asn Ser Asn Leu Val Gly Ala Ala  
 275 280 285  
 His Glu Glu Leu Gln Gln Ser Arg Ile Arg Ile Asp Ser Leu Ser Ala  
 290 295 300  
 Gln Leu Ser Gln Leu Gln Lys Gln Leu Ala Ala Lys Glu Ala Lys Leu  
 305 310 315 320  
 Arg Asp Leu Glu Asp Ser Leu Ala Arg Glu Arg Asp Thr Ser Arg Arg  
 325 330 335  
 Leu Leu Ala Glu Lys Glu Arg Glu Met Ala Glu Met Arg Ala Arg Met  
 340 345 350  
 Gln Gln Gln Leu Asp Glu Tyr Gln Glu Leu Leu Asp Ile Lys Leu Ala  
 355 360 365  
 Leu Asp Met Glu Ile His Ala Tyr Arg Lys Leu Leu Glu Gly Glu Glu  
 370 375 380  
 Glu Arg Leu Arg Leu Ser Pro Ser Pro Thr Ser Gln Arg Ser Arg Gly  
 385 390 395 400  
 Arg Ala Ser Ser His Ser Ser Gln Thr Gln Gly Gly Gly Ser Val Thr  
 405 410 415  
 Lys Lys Arg Lys Leu Glu Ser Thr Glu Ser Arg Ser Ser Phe Ser Gln  
 420 425 430

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His Ala Arg Thr Ser Gly Arg Val Ala Val Glu Glu Val Asp Glu Glu  
435 440 445

Gly Lys Phe Val Arg Leu Arg Asn Lys Ser Asn Glu Asp Gln Ser Met  
450 455 460

Gly Asn Trp Gln Ile Lys Arg Gln Asn Gly Asp Asp Pro Leu Leu Thr  
465 470 475 480

Tyr Arg Phe Pro Pro Lys Phe Thr Leu Lys Ala Gly Gln Val Val Thr  
485 490 495

Ile Trp Ala Ala Gly Ala Gly Ala Thr His Ser Pro Pro Thr Asp Leu  
500 505 510

Val Trp Lys Ala Gln Asn Thr Trp Gly Cys Gly Asn Ser Leu Arg Thr  
515 520 525

Ala Leu Ile Asn Ser Thr Gly Glu Glu Val Ala Met Arg Lys Leu Val  
530 535 540

Arg Ser Val Thr Val Val Glu Asp Asp Glu Asp Glu Asp Gly Asp Asp  
545 550 555 560

Leu Leu His His His His Val Ser Gly Ser Arg Arg  
565 570

<210> 29  
<211> 10  
<212> PRT  
<213> Human

<400> 29

Asn Leu Leu Glu Lys Asp Tyr Phe Gly Leu  
1 5 10

<210> 30  
<211> 10  
<212> PRT  
<213> Human

<400> 30

Val Leu Phe Asp Leu Val Cys Glu His Leu  
1 5 10

<210> 31  
<211> 9  
<212> PRT

&lt;213&gt; Human

&lt;400&gt; 31

Lys Leu Gln His Pro Asp Met Leu Val  
 1 5

&lt;210&gt; 32

&lt;211&gt; 9

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 32

Lys Met Leu Asp Ala Glu Asp Ile Val  
 1 5

&lt;210&gt; 33

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 33

Lys Met Thr Leu Gly Met Ile Trp Thr Ile  
 1 5 10

&lt;210&gt; 34

&lt;211&gt; 9

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 34

Phe Met Pro Ser Glu Gly Lys Met Val  
 1 5

&lt;210&gt; 35

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 35

Lys Leu Ala Ser Asp Leu Leu Glu Trp Ile  
 1 5 10

&lt;210&gt; 36

&lt;211&gt; 9

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 36

Gly Leu Val Thr Phe Gln Ala Phe Ile  
 1 5

<210> 37  
 <211> 10  
 <212> PRT  
 <213> Human

<400> 37

Cys Gln Leu Glu Ile Asn Phe Asn Ser Val  
 1 5 10

<210> 38  
 <211> 10  
 <212> PRT  
 <213> Human

<400> 38

Trp Leu Ala Ala Val Thr Lys Gln Asn Val  
 1 5 10

<210> 39  
 <211> 10  
 <212> PRT  
 <213> Human

<400> 39

Ile Leu Pro Phe Arg Val Ile Pro Leu Val  
 1 5 10

<210> 40  
 <211> 9  
 <212> PRT  
 <213> Human

<400> 40

Ser Leu Leu Ala Gln Lys Ile Glu Val  
 1 5

<210> 41  
 <211> 9  
 <212> PRT  
 <213> Human

<400> 41

Lys Leu Asn Tyr Ser Asp His Asp Val  
 1 5

<210> 42  
 <211> 9  
 <212> PRT  
 <213> Human

<400> 42

Lys Leu Leu Gly Gly Gln Ile Gly Leu

1 5

<210> 43  
 <211> 10  
 <212> PRT  
 <213> Human

<400> 43

Ser Leu Leu Gly Cys Arg His Tyr Glu Val  
 1 5 10

<210> 44  
 <211> 10  
 <212> PRT  
 <213> Human

<400> 44

Tyr Leu Ser Gln Glu His Gln Gln Gln Val  
 1 5 10

<210> 45  
 <211> 10  
 <212> PRT  
 <213> Human

<400> 45

Lys Val Met Asp Arg Pro Gly Asn Tyr Val  
 1 5 10

<210> 46  
 <211> 9  
 <212> PRT  
 <213> Human

<400> 46

Ala Leu Ile Glu Gln Trp Asn Pro Val  
 1 5

<210> 47  
 <211> 9  
 <212> PRT  
 <213> Human

<400> 47

Ile Ile Thr Ala Phe Asn Phe Pro Val  
 1 5

<210> 48  
 <211> 9  
 <212> PRT  
 <213> Human



&lt;400&gt; 48

Phe Glu Gln Glu Asn Asp Trp Trp Val  
1 5

&lt;210&gt; 49

&lt;211&gt; 9

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 49

Tyr Leu Gly Ala Lys Pro Trp Cys Leu  
1 5

&lt;210&gt; 50

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 50

Cys Leu Gln Thr Gly Phe Ala Ile Gly Val  
1 5 10

&lt;210&gt; 51

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 51

Lys Leu Leu Glu Gly Glu Glu Glu Arg Leu  
1 5 10

&lt;210&gt; 52

&lt;211&gt; 9

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 52

Lys Leu Val Arg Ser Val Thr Val Val  
1 5

&lt;210&gt; 53

&lt;211&gt; 9

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 53

Arg Leu Ala Asp Ala Leu Gln Glu Leu  
1 5